

SCORE Search Results Details for Application  
10668767 and Search Result us-10-668-767-  
128\_copy\_1\_1700.p2n.rnpbm.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10668767 and Search Result us-10-668-767-128\_copy\_1\_1700.p2n.rnpbm.

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OM protein - nucleic search, using frame\_plus\_p2n model

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Run on:      October 23, 2006, 08:16:57 ; Search time 3663 Seconds
              (without alignments)
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                  Ygapop 10.0 , Ygapext 0.5
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                  Delop  6.0 , Delext 7.0
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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Published Applications NA Main:\*

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 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	8985	100.0	15387	8	US-10-668-767-127	Sequence 127, App
2	8970	99.8	15405	8	US-10-668-767-129	Sequence 129, App
3	8931.5	99.4	15429	8	US-10-668-767-143	Sequence 143, App
4	8872.5	98.7	15679	8	US-10-668-767-1	Sequence 1, Appli
5	8734	97.2	15303	8	US-10-668-767-145	Sequence 145, App
6	7112	79.2	15413	8	US-10-668-767-7	Sequence 7, Appli
7	6964.5	77.5	16363	8	US-10-668-767-9	Sequence 9, Appli
8	6920.5	77.0	15315	8	US-10-668-767-5	Sequence 5, Appli
9	6887	76.6	15606	13	US-11-097-143-22562	Sequence 22562, A
10	6841.5	76.1	15845	8	US-10-668-767-3	Sequence 3, Appli
c 11	6196.5	69.0	24236	13	US-11-097-143-22561	Sequence 22561, A
12	3817	42.5	14302	8	US-10-276-774-552	Sequence 552, App
13	3817	42.5	15731	10	US-10-887-553A-490	Sequence 490, App
14	3660	40.7	15359	8	US-10-276-774-500	Sequence 500, App
15	3660	40.7	15359	10	US-10-887-553A-489	Sequence 489, App
16	3660	40.7	15359	10	US-10-450-763-4960	Sequence 4960, Ap
17	3655	40.7	15563	8	US-10-764-425-48	Sequence 48, Appl
18	3655	40.7	15563	10	US-10-887-553A-491	Sequence 491, App
19	3653.5	40.7	14620	15	US-11-044-111-17	Sequence 17, Appl
20	3640	40.5	15564	15	US-11-000-688-1500	Sequence 1500, Ap
21	3606	40.1	15583	10	US-10-450-763-12305	Sequence 12305, A
22	3606	40.1	15820	10	US-10-450-763-23337	Sequence 23337, A
23	3536	39.4	15453	9	US-10-723-860-5796	Sequence 5796, Ap
24	3525	39.2	4078	7	US-10-305-720-1154	Sequence 1154, Ap
25	2709.5	30.2	3168	15	US-11-044-111-8	Sequence 8, Appli
26	698.5	7.8	1800	10	US-10-450-763-23334	Sequence 23334, A
27	603	6.7	717	15	US-11-044-111-18	Sequence 18, Appl
28	576.5	6.4	636	15	US-11-044-111-19	Sequence 19, Appl
29	424	4.7	524	15	US-11-044-111-20	Sequence 20, Appl
30	327	3.6	10129	15	US-11-044-111-21	Sequence 21, Appl
31	324.5	3.6	597	7	US-10-029-386-2405	Sequence 2405, Ap
32	324	3.6	11806	8	US-10-367-094-123	Sequence 123, App
33	323.5	3.6	10716	16	US-11-136-527-2862	Sequence 2862, Ap
34	320.5	3.6	12850	8	US-10-367-094-126	Sequence 126, App
35	320	3.6	321	7	US-10-029-386-16105	Sequence 16105, A

36	319.5	3.6	10524	6	US-10-171-581-184	Sequence 184, App
37	319.5	3.6	10524	8	US-10-240-425-1212	Sequence 1212, Ap
38	318.5	3.5	479	12	US-10-301-480-3997	Sequence 3997, Ap
39	318.5	3.5	479	12	US-10-301-480-617406	Sequence 617406,
c 40	318.5	3.5	535	6	US-10-027-632-59310	Sequence 59310, A
c 41	318.5	3.5	535	7	US-10-027-632-59310	Sequence 59310, A
c 42	318.5	3.5	643	6	US-10-027-632-51124	Sequence 51124, A
c 43	318.5	3.5	643	7	US-10-027-632-51124	Sequence 51124, A
44	299	3.3	8806	8	US-10-152-319A-1612	Sequence 1612, Ap
45	299	3.3	8806	16	US-11-036-196-1612	Sequence 1612, Ap

## ALIGNMENTS

## RESULT 1

US-10-668-767-127

; Sequence 127, Application US/10668767

; Publication No. US20040171114A1

; GENERAL INFORMATION:

; APPLICANT: Caspar, Timothy

; APPLICANT: Cordova, Daniel

; APPLICANT: Gutteridge, Steven

; APPLICANT: Rauh, James

; APPLICANT: Smith, Rejane

; APPLICANT: Tao, Yong

; APPLICANT: Wu, Lihong

; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors

; FILE REFERENCE: BB1533 US NA

; CURRENT APPLICATION NUMBER: US/10/668,767

; CURRENT FILING DATE: 2003-09-23

; PRIOR APPLICATION NUMBER: 60/412,795

; PRIOR FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: 60/427,324

; PRIOR FILING DATE: 2002-11-18

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 127

; LENGTH: 15387

; TYPE: DNA

; ORGANISM: Heliothis virescens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(15384)

; OTHER INFORMATION:

; FEATURE:

; OTHER INFORMATION: pXL-Hv7

US-10-668-767-127

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**SCORE Search Results Details for Application 10668767 and Search Result us-10-668-767-128\_copy\_1\_1700.p2n.rnpbn.**

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OM protein - nucleic search, using frame\_plus p2n model

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Perfect score: 8985  
Sequence: 1 MAEAEGGASEODDVSFLRTE.....LQIELGRSATSLPLSAAVLP 1700

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Scoring table:  BLOSUM62
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
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1	3655	40.7	15563	8	US-11-266-748A-57467	Sequence 57467, A
2	319.5	3.6	10524	8	US-11-266-748A-29244	Sequence 29244, A
3	280.5	3.1	8833	6	US-10-505-928-785	Sequence 785, App
4	280.5	3.1	8833	8	US-11-266-748A-29245	Sequence 29245, A
5	280.5	3.1	8833	8	US-11-266-748A-31810	Sequence 31810, A
6	280.5	3.1	8833	8	US-11-266-748A-56209	Sequence 56209, A
7	279.5	3.1	8404	8	US-11-266-748A-28705	Sequence 28705, A
8	235.5	2.6	1406	8	US-11-266-748A-31954	Sequence 31954, A
9	193.5	2.2	2084	8	US-11-266-748A-31119	Sequence 31119, A
10	193.5	2.2	3473	8	US-11-266-748A-22595	Sequence 22595, A
11	193.5	2.2	3473	8	US-11-266-748A-22596	Sequence 22596, A
12	183.5	2.0	4226	8	US-11-293-697-1236	Sequence 1236, Ap
13	180.5	2.0	1450	8	US-11-266-748A-186649	Sequence 186649,
14	180.5	2.0	1937	1	US-09-949-925-61	Sequence 61, Appl
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c 18	176	2.0	1000	8	US-11-266-748A-474794	Sequence 474794,
19	155	1.7	1991	8	US-11-266-748A-251793	Sequence 251793,
c 20	155	1.7	1991	8	US-11-266-748A-312310	Sequence 312310,
c 21	154.5	1.7	583	8	US-11-266-748A-377158	Sequence 377158,
22	154.5	1.7	583	8	US-11-266-748A-460537	Sequence 460537,
23	154	1.7	2667	8	US-11-266-748A-23535	Sequence 23535, A
24	149	1.7	2947	8	US-11-266-748A-26565	Sequence 26565, A
25	144.5	1.6	349	8	US-11-266-748A-373619	Sequence 373619,
c 26	144.5	1.6	349	8	US-11-266-748A-456998	Sequence 456998,
27	143	1.6	813	8	US-11-266-748A-193768	Sequence 193768,
28	143	1.6	813	8	US-11-266-748A-227276	Sequence 227276,
29	140.5	1.6	6926	8	US-11-266-748A-24639	Sequence 24639, A
30	139	1.5	8637	8	US-11-266-748A-31695	Sequence 31695, A
31	138	1.5	2617	8	US-11-266-748A-24756	Sequence 24756, A
32	138	1.5	3749	6	US-10-449-902-7917	Sequence 7917, Ap
33	137.5	1.5	1886	9	US-11-218-305-18063	Sequence 18063, A
34	136.5	1.5	14771	8	US-11-266-748A-56688	Sequence 56688, A
35	133.5	1.5	2869	6	US-10-449-902-12735	Sequence 12735, A
36	133.5	1.5	10881	8	US-11-266-748A-23861	Sequence 23861, A
37	133.5	1.5	14315	8	US-11-266-748A-57331	Sequence 57331, A
38	132	1.5	3354	7	US-11-299-286-511	Sequence 511, App
39	131	1.5	1603	8	US-11-266-748A-184497	Sequence 184497,
40	131	1.5	1603	8	US-11-266-748A-192003	Sequence 192003,
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c 45	130.5	1.5	3879	8	US-11-266-748A-128006	Sequence 128006,

## ALIGNMENTS

## RESULT 1

US-11-266-748A-57467

; Sequence 57467, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 57467

; LENGTH: 15563

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-11-266-748A-57467

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Qy      22 MetValCysLeuSerCysThrAlaThr-----GlyGluArgValCysLeuAla 37
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**SCORE Search Results Details for Application 10668767 and Search Result us-10-668-767-128\_copy\_1\_1700.p2n.rni.**

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<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10668767 and Search Result us-10-668-767-128\_copy\_1\_1700.p2n.rni.

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OM protein - nucleic search, using frame\_plus p2n model

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Run on:      October 23, 2006, 08:16:53 ; Search time 654 Seconds
              (without alignments)
              7295.608 Million cell updates/sec
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```
Title:          US-10-668-767-128_COPY_1_1700
Perfect score:  8985
Sequence:       1 MAEAEGGASEQDDVSFLRTE.....LQIELGRSATSLPLSAAVLP 1700
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Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop  6.0 , Delext  7.0
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Searched: 1403666 seqs, 93554401 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
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 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score					
1	3667.5	40.8	15378	3	US-08-785-420-1	Sequence 1, Appli
2	3606	40.1	15572	3	US-09-424-783-1	Sequence 1, Appli
3	3525	39.2	4078	3	US-09-016-434-1154	Sequence 1154, Ap
4	313.5	3.5	8024	3	US-09-949-016-2978	Sequence 2978, Ap
5	292.5	3.3	9610	3	US-09-566-921-45	Sequence 45, Appl
6	289	3.2	8791	7	PCT-US96-01735-5	Sequence 5, Appli
7	286	3.2	1050	2	US-08-480-481-3	Sequence 3, Appli
8	285	3.2	1050	2	US-08-480-481-4	Sequence 4, Appli
9	280.5	3.1	8833	4	US-09-880-107-3272	Sequence 3272, Ap
10	279	3.1	9848	3	US-09-385-222A-3	Sequence 3, Appli
11	252	2.8	900	2	US-08-480-481-6	Sequence 6, Appli
12	222	2.5	1812	3	US-09-385-222A-1	Sequence 1, Appli
c 13	186	2.1	837	3	US-09-270-767-13497	Sequence 13497, A
14	162	1.8	1598	3	US-08-785-420-3	Sequence 3, Appli
15	153	1.7	15071	3	US-09-710-279-2963	Sequence 2963, Ap
16	152.5	1.7	3281	3	US-09-270-767-13398	Sequence 13398, A
17	148	1.6	2600	3	US-09-949-016-4202	Sequence 4202, Ap
18	145	1.6	3223	2	US-07-980-528-1	Sequence 1, Appli
19	140	1.6	30549	3	US-09-134-001C-322	Sequence 322, App
20	139	1.5	3465	3	US-09-134-000C-2717	Sequence 2717, Ap
21	138	1.5	536165	3	US-09-214-808-1	Sequence 1, Appli
22	136.5	1.5	13187	3	US-09-949-016-5062	Sequence 5062, Ap
23	136.5	1.5	14770	3	US-09-220-132-30	Sequence 30, Appl
24	136.5	1.5	14770	3	US-09-949-016-1107	Sequence 1107, Ap
25	136.5	1.5	176006	3	US-09-949-016-16804	Sequence 16804, A
26	136.5	1.5	253375	3	US-09-949-016-12849	Sequence 12849, A
c 27	134.5	1.5	7096	3	US-09-221-017B-373	Sequence 373, App
28	133.5	1.5	37948	3	US-09-251-645-11	Sequence 11, Appl
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31	132.5	1.5	2576	2	US-08-463-483A-35	Sequence 35, Appl
32	132.5	1.5	2576	2	US-08-471-046A-35	Sequence 35, Appl
33	132.5	1.5	2576	2	US-08-470-566B-35	Sequence 35, Appl
34	132.5	1.5	2576	2	US-08-469-334-35	Sequence 35, Appl
35	132.5	1.5	2576	3	US-09-300-529-35	Sequence 35, Appl
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## ALIGNMENTS

## RESULT 1

US-08-785-420-1

; Sequence 1, Application US/08785420

; Patent No. 6001976

; GENERAL INFORMATION:

; APPLICANT: MacLennan, David H

; APPLICANT: O'Brien, Peter J.

; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT

; TITLE OF INVENTION: HYPERTHERMIA

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bell, Seltzer, Park &amp; Gibson

; STREET: P.O. Drawer 34009

; CITY: Charlotte,

; STATE: No. 6001976th Carolina 28234

; COUNTRY: U.S.A.

; ZIP: 28234

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/785,420

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/249,388

; FILING DATE:

; APPLICATION NUMBER: US 08/030,159

; FILING DATE: 15-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Layton, Jr., Samuel G.

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; REFERENCE/DOCKET NUMBER: 3477-73

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 704-377-1561

; TELEFAX: 704-334-2014

; TELEX: 57-5102

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15378 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; IMMEDIATE SOURCE:

; CLONE: Porcine RYR1 Gene

; POSITION IN GENOME:

; UNITS: bp

US-08-785-420-1